

GenCore version 5.1.4-p5\_4578  
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OM protein - protein search, using sw model

Run on: May 9, 2003, 17:00:40 ; Search time 29.3505 Seconds

(without alignments)  
2351.779 Million cell updates/sec

Title: US-09-446-634A-22

Perfect score: 1804  
Sequence: 1 MGITPLPLVLSVARS.....KDTSDSENPNRRTIOSLY 335

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

- 1: SP\_ARCHAEA:\*
- 2: SP\_BACTERIA:\*
- 3: SP\_FUNGI:\*
- 4: SP\_HUMAN:\*
- 5: SP\_INVERTEBRATE:\*
- 6: SP\_MAMMAL:\*
- 7: SP\_MHC:\*
- 8: SP\_ORNITHINE:\*
- 9: SP\_PHAGE:\*
- 10: SP\_PLANT:\*
- 11: SP\_PROTOZOA:\*
- 12: SP\_VIRUS:\*
- 13: SP\_VERTEBRATE:\*
- 14: SP\_UNCLASSIFIED:\*
- 15: SP\_VIRUS:\*
- 16: SP\_BACTERIOPHAGE:\*
- 17: SP\_ARCHAEA:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1552	86.0	331	6	O9TSM4 macaca fasc
2	1531	84.9	331	6	O9BDN0 macaca neme
3	1521	84.3	331	6	O9BDN4 macaca neme
4	1509	83.6	333	6	O9BDP2 macaca mola
5	1500	83.1	331	6	O9GK36 macaca asse
6	1492.5	82.7	334	6	O9GK40 macaca mola
7	1439.5	79.8	310	6	O9GK28 macaca arc
8	1377.5	76.4	328	6	O9BDP0 macaca arc
9	1057.5	58.3	320	6	O9XS29 macaca arc
10	1052	58.3	319	6	O9TSM2 macaca arc
11	967	53.6	327	6	O9TSM3 macaca arc
12	614.5	34.1	263	6	O9XS60 macaca arc
13	481.5	26.7	150	11	O9R330 macaca arc
14	478	26.3	147	6	O9S032 macaca arc
15	470	26.1	285	13	O9DGH7 macaca arc
16	463.5	25.7	312	13	O9DGH8 macaca arc

17	429.5	23.8	124	6	O9S031 macaca arc
18	286	15.9	65	6	O9S049 macaca arc
19	246	13.6	357	13	O9DGH3 macaca arc
20	226.5	12.6	368	13	O9DGH4 macaca arc
21	212.5	11.8	438	13	O9DGH5 macaca arc
22	208.5	11.6	387	13	O9DGH6 macaca arc
23	199	11.0	368	13	O9DGH7 macaca arc
24	198	11.0	383	6	O9XS28 macaca arc
25	189	10.5	368	13	O9DGH2 macaca arc
26	180	10.0	276	13	O9DGH3 macaca arc
27	179	9.9	401	13	O9DGH7 macaca arc
28	171	9.5	413	11	O9S041 macaca arc
29	170.5	9.5	446	6	O9S043 macaca arc
30	168	9.3	186	12	O9YB87 macaca arc
31	163	9.0	186	12	O9YB84 macaca arc
32	161.5	9.0	169	11	O9JRE0 macaca arc
33	161.5	9.0	326	12	O57120 macaca arc
34	161	8.9	186	12	O72735 macaca arc
35	161	8.9	186	12	O91185 macaca arc
36	159.5	8.8	350	12	O57123 macaca arc
37	158.5	8.8	278	6	O9S034 macaca arc
38	155.5	8.6	387	11	O9VD70 macaca arc
39	153.5	8.5	326	12	O57122 macaca arc
40	153	8.5	349	12	O57098 macaca arc
41	153	8.5	349	12	O8UYA7 macaca arc
42	153	8.5	349	12	O57284 macaca arc
43	152	8.4	347	12	O57119 macaca arc
44	151.5	8.4	349	12	O57100 macaca arc
45	151.5	8.4	349	12	O57102 macaca arc

ALIGNMENTS

RESULT 1	ID	Q9TSM4	PRELIMINARY:	PRT:	331 AA.
AC	O9TSM4	01-MAR-2000 (TREMREL. 13, Created)			
DT	01-MAR-2000 (TREMREL. 13, Last sequence update)				
DT	01-DEC-2001 (TREMREL. 19, Last annotation update)				
DE	Death receptor Fas (APO-1/CD95).				
GN	FAS.				
OS	Macaca fascicularis (Crib eating macaque) (Cynomolgus monkey).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;				
OC	Cercopithecoidea; Macaca.				
OX	NCBI_TaxID:9541;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-20237686; PubMed-10773350;				
RA	Murayama Y., Terao K., Inoue-Murayama M.;				
RT	"Molecular cloning and characterization of cynomolgus monkey Fas.";				
RL	Hum. Immunol. 61:474-485(2000).				
DR	EMBL; AB031430; BAA83551.1; -				
DR	HSSP; P25445; 1DDF.				
DR	InterPro; IPR000488; Death.				
DR	InterPro; IPR001368; TNFR-C6.				
DR	Pfam; PF00531; death_1.				
DR	Pfam; PF00020; TNFR_C6; 2.				
DR	SMART; SM00058; DEATH_1.				
DR	SMART; SM00058; TNFR_2.				
DR	PROSITE; PSS0017; DEATH_DOMAIN; 1.				
DR	PROSITE; PSS0052; TNFR_NGFR_1; 1.				
DR	PROSITE; PSS0050; TNFR_NGFR_2; 2.				
KW	Receptor.				
SO	SEQUENCE	331 AA; 37265 MW; 06617508081B05DF CRC64;			
Query Match		86.0%; Score 1552; DB 6; Length 331;			
Best Local Similarity		87.2%; Pred. No. 2.2e-121;			
Matches 292; Conservative		14; Mismatches 25; Indels 4; Gaps 2;			
OY	1 MGITPLPLVLSVARSVNAQVTDINSKLEIRKTVTVETONLECHHDCQFCH 60				

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# OM protein - protein search, using SW model

Run on: May 9, 2003, 16:57:39 : Search time 54.3354 Seconds  
(without alignments)  
801.926 Million cell updates/sec

Title: US-09-446-634a-23  
Perfect score: 1804  
Sequence: 1 MLMWAVLPVLVAGSQLRVH.....KDLGRSTPDGTGNEGSCCLE 327

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues  
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: A\_Geneseq\_101002.\*  
1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*  
5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.\*  
6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.\*  
7: /SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.\*  
8: /SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*  
9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*  
10: /SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.\*  
11: /SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*  
12: /SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*  
13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*  
14: /SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.\*  
15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.\*  
16: /SID52/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.\*  
17: /SID52/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.\*  
18: /SID52/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1804	100.0	327	14 AAR1688
2	1804	100.0	327	16 AAR78611
3	1804	100.0	327	17 AAR92530
4	1804	100.0	327	21 AAB9344
5	1800	99.8	327	20 AAB6241
6	1001	55.5	576	16 AAR78613
7	981	54.4	592	17 AAR92527
8	977	54.2	169	16 AAR78612
9	863.5	47.9	669	19 AAB6484
10	856	47.5	335	13 AAR28084

11	856	47.5	325	16 AAR78606	Human Fas protein.
12	856	47.5	335	17 AAR98681	Human Fas antigen.
13	856	47.5	335	17 AAR92528	hfas from plasmid
14	856	47.5	335	19 AAB50289	Human Fas antigen.
15	856	47.5	335	19 AAB49104	Fas protein. Mamm
16	856	47.5	335	21 AAB19341	Amino acid encodin
17	856	47.5	335	21 AAB80135	CD-95 (FAS/APC-1)
18	856	47.5	335	22 AAB50517	Human tumour necro
19	844	46.8	335	21 AAB50517	Human Fas receptor
20	825	45.7	331	22 AAB50893	Human Fas receptor
21	810.5	44.9	314	16 AAR78238	Fas-delta-TM. Hom
22	810.5	44.9	314	17 AAR98682	Human Fas soluble
23	801.5	44.4	314	20 AAB98070	Soluble Fas recept
24	676.5	37.5	170	21 AAB36228	Rat Fas receptor.
25	645	35.8	281	21 AAB26982	Human Fas. Homo s
26	585	32.4	219	22 AAB66978	Fas protein. Unid
27	530	29.4	173	21 AAB36229	Human Fas receptor
28	530	29.4	600	16 AAR78610	Expression vector
29	523	28.0	237	21 AAB53420	Human colon cancer
30	520	28.8	600	17 AAR92525	Fas antigen fl.
31	494.5	27.4	144	18 AAB50288	Human Fas antigen
32	494.5	27.4	159	18 AAB50288	Human Fas antigen
33	494.5	27.4	376	18 AAB50287	Human Fas antigen
34	494.5	27.4	376	19 AAB60037	Antigenic peptide
35	482	26.7	86	23 AAB91259	Nucleic acid selec
36	341	18.9	431	22 AAB97650	CD44extrAFASm/cy
37	340.5	18.9	920	22 AAB97652	Flt-1extrAFASm/cy
38	339	18.8	927	22 AAB97652	Flt-1extrAFASm/cy
39	332	18.4	436	21 AAB91026	Apoptobody3sc fusl
40	319.5	17.7	436	22 AAB97651	CD44extrAFASm/cy
41	305.5	16.9	149	17 AAB95683	Human Fas soluble
42	281	15.6	121	23 AAB81752	Tumour necrosis fa
43	278.5	15.4	111	23 AAB81750	Tumour necrosis fa
44	226	12.5	84	22 AAB97654	Fas/APC-1/CD95 Dea
45	220	12.2	84	19 AAB62178	Fas-R protein frag

## ALIGNMENTS

RESULT 1	AAAR1688	AAAR1688 standard; Protein; 327 AA.
XX	AAAR1688;	
AC	AAAR1688;	
DT	19-APR-1994	(first entry)
XX		
DE	Murine Fas.	
XX		
KW	Murine; Fas; human; macrophage; cell strain; BM3.	
XX		
OS	Mus musculus.	
XX		
PN	JP05219959-A.	
XX		
PD	31-MUG-1993.	
XX		
PF	14-FEB-1992;	92JP-0028090.
XX		
PR	14-FEB-1992;	92JP-0028090.
XX		
PA	(OSAB-) ZH OSAKA BIOSCIENCE KENKYUSHO.	
XX		
DR	WPI: 1993-308326/39.	
XX	N-PSDB: AAO48008.	
XX		
PT	DNA hybridising with sequence coding for human FAS protein - 1s	
XX	prepd. from e.g. BM3 cell of mouse macrophage cell	
XX		
PS	Claim 1; Page 6-7; 8pp; Japanese.	
XX		
CC	This sequence represents the murine Fas protein. The cDNA encoding	

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OM protein - protein search, using SW model

Run on: May 9, 2003, 17:02:31; Search time 28.1556 seconds  
(without alignments)  
1116.509 Million cell updates/sec

Title: US-09-446-634A-23

Perfect score: 1804  
Sequence: 1 MIMINAVLPVLVAGSOLRVH.....KDLGKSPDPTGNEGQCLE 327

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: PIR\_73:\*

- 1: PIR1:\*
- 2: PIR2:\*
- 3: PIR3:\*
- 4: PIR4:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1804	100.0	327	2	A46484
2	1058.5	98.7	324	2	JC2395
3	856	47.5	335	2	A40036
4	810.5	44.9	314	2	I37383
5	305.5	16.9	149	2	S58662
6	203.5	11.3	271	2	S12783
7	202	11.2	272	2	I48700
8	194.5	10.8	277	2	A60771
9	189.5	10.5	455	1	GOHRT1
10	185	10.3	454	1	GOHRT1
11	183	10.1	260	1	A46517
12	179.5	10.0	435	2	I34182
13	179	9.9	461	1	GOHRT1
14	171	9.5	277	2	I37552
15	169	9.4	461	2	JC4302
16	167	9.3	250	1	A49053
17	165.5	9.2	416	1	A46476
18	165	9.1	305	2	A49053
19	165	9.1	349	2	D72175
20	163	9.0	348	2	T28623
21	163	9.0	349	2	D38558
22	154.5	8.6	425	1	A26431
23	154.5	8.6	595	2	A42086
24	148	8.2	461	1	A43556
25	141	7.8	427	1	GOHUN
26	135.5	7.5	677	2	C42125
27	126.5	7.0	1372	2	T25933
28	126	7.0	493	2	JC5486
29	123.5	6.8	459	2	I48854

30	122.5	6.8	255	2	I38426
31	122	6.8	103	2	I37384
32	120.5	6.7	1111	2	T26972
33	119.5	6.6	474	2	B38634
34	119	6.6	2823	2	T23004
35	119	6.6	2823	2	F87908
36	119	6.6	3102	2	T43291
37	116.5	6.5	325	2	B43692
38	116	6.4	3122	2	S18253
39	115.5	6.4	1820	2	T27283
40	115.5	6.4	1816	1	S68960
41	115.5	6.4	3672	2	T23433
42	115.5	6.4	3704	2	T27316
43	115	6.4	1274	2	T42017
44	114	6.3	626	2	T04895
45	114	6.3	686	2	JC7569

lymphocyte activat  
FAS soluble protei  
hypothetical prote  
tumor necrosis fac  
hypothetical prote  
protein T22A3.8 (1  
laminin alpha chain  
laminin alpha-1 ch  
hypothetical prote  
laminin alpha-4 ch  
hypothetical prote  
probable laminin a  
cysteine rich prot  
vacuolar sorting r  
delta-4 protein -

ALIGNMENTS

RESULT 1  
A46484  
A:Species: Mus musculus (house mouse)  
C:Date: 18-Jun-1993 #sequence revision 18-Nov-1994 #text change 05-Nov-1999  
C:Accession: A46484, A47254  
J:Watanabe-Fukunaga, R.; Brannan, C.I.; Itoh, N.; Yonehara, S.; Copeland, N.G.; Jenk  
J. Immunol. 148, 1274-1279, 1992  
A:Title: The CDNA structure, expression, and chromosomal assignment of the mouse Fas  
A:Reference number: A46484; MUID:9218151; PMID:1371136  
A:Accession: A46484  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1327<CRAT>  
A:Cross-References: GB:M33649; NID:9193225; PID:AAA37593.1; PID:9193226  
A:Experimental source: EMB3 macrophage cell line  
A:Note: Sequence extracted from NCBI backbone (NCBIN:81544, NCBI:81545)  
R:Adachi, M.; Watanabe-Fukunaga, R.; Nagata, S.  
Proc. Natl. Acad. Sci. U.S.A. 90, 1756-1760, 1993  
A:Title: Aberrant transcription caused by the insertion of an early transposable ele  
F:44-79/Domain: NGF receptor repeat homology <NGF>  
A:Reference number: A47254; MUID:93189576; PMID:7680478  
A:Accession: A47254  
A:Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 196<KDA>  
A:Cross-References: GB:S56450; NID:9298505; PID:AAA25700.1; PID:9298506  
A:Experimental source: MRL lpr/lpr  
A:Note: Sequence extracted from NCBI backbone (NCBIN:126850, NCBIN:126853, NCBIN:126  
C:Superfamily: NGF receptor repeat homology  
C:Keywords: transmembrane protein  
F:44-79/Domain: NGF receptor repeat homology <NGF>  
Query Match 100.0%; Score 1804; DB 2; Length 327;  
Best Local Similarity 100.0%; Pred. No. 6.9e-122;  
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MIMINAVLPVLVAGSOLRVHVTGNTSISLKLRRVETDKNSSELYGGFFCQPCQ 60  
DB 1 MIMINAVLPVLVAGSOLRVHVTGNTSISLKLRRVETDKNSSELYGGFFCQPCQ 60

QY 61 PGKRYEDCKNMGSPFCAPCTEGREYMDKNHAKRCRCLDEHGLEVEFNCTN 120  
DB 61 PGKRYEDCKNMGSPFCAPCTEGREYMDKNHAKRCRCLDEHGLEVEFNCTN 120

QY 121 TKKCKPDYDSDPSCHEVCRCASCHGTLPECTATSTNCRKOSPNNRLMLTLIVLI 180  
DB 121 TKKCKPDYDSDPSCHEVCRCASCHGTLPECTATSTNCRKOSPNNRLMLTLIVLI 180

QY 181 PLVFYIKRRRKCKMRKRRDDPSRTSSRETIIPNANSLSLSKYIPRIADMD7YCAKF 240  
DB 181 PLVFYIKRRRKCKMRKRRDDPSRTSSRETIIPNANSLSLSKYIPRIADMD7YCAKF 240

QY 241 ARENNKEGKIDEIMHDSIQDTAEOKVOLLICMYOSHGKSDAYODLIFKIKAKRCRRLD 300  
 DB 241 ARENNKEGKIDEIMHDSIQDTAEOKVOLLICMYOSHGKSDAYODLIFKIKAKRCRRLD 300  
 QY 301 KPODMVOKDLKSTPTDGENEGOCLE 327  
 DB 301 KPODMVOKDLKSTPTDGENEGOCLE 327

## RESULT 2

JC2395  
 Fas antigen precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 05-Nov-1995  
 C:Accession: JC2395; PC2246  
 R:Klimstra, A.; Wakatsuki, T.; Yamamoto, M.  
 Biochem. Biophys. Res. Commun. 198, 666-674, 1994  
 A:Title: A variant mRNA species encoding a truncated form of Fas antigen in the rat liver  
 A:Reference number: JC2395; MUID:94128114; PMID:7507668  
 A:Accession: JC2395  
 A:Molecule type: mRNA  
 A:Residues: 1-324 <RIN>  
 A:Cross-references: DBJ:D26112; NID:9468486; PID:BA05108.1; PID:d1005650; PID:9468487  
 A:Experimental source: thymus  
 A:Accession: PC2246  
 A:Molecule type: mRNA  
 A:Residues: 1-62, 'RFT', <RT2>  
 A:Cross-references: DBJ:D26113; NID:9468488; PID:BA05109.1; PID:d1005651; PID:9468488  
 A:Experimental source: liver  
 C:Genetics:  
 A:Introns: 62/1  
 C:Superfamily: NGF receptor repeat homology  
 C:Keywords: transmembrane protein  
 F:1-21/Domain: signal sequence #status predicted <SIG>  
 F:22-324/Product: Fas antigen #status predicted <NMT>  
 F:44-79/Domain: NGF receptor repeat homology <NGF>  
 F:81-124/Domain: NGF receptor repeat homology <NGF>  
 F:171-188/Domain: transmembrane #status predicted <TM>

## Query Match

58.7% Score 1058.5; DB 2: Length 324;  
 Best Local Similarity: 61.1% Pred. No. 156-68;  
 Matches 201; Conservative 41; Mismatches 80; Indels 7; Gaps 3;

QY 1 MIMTAVLPVLAGSGLRVHGTGNSISLKLRRVHETDKNCSEGLYOGGPFCCQ 60  
 DB 1 MIMTAVLPVLAGSGLRVHGTGNSISLKLRRVHETDKNCSEGLYOGGPFCCQ 60  
 QY 61 PGRKRVKDCCTTSGAFTCHPCTBEETDRKHSKCRCAFCDEGHELEVENCTRTON 120  
 DB 61 PGRKRVKDCCTTSGAFTCHPCTBEETDRKHSKCRCAFCDEGHELEVENCTRTON 120  
 QY 121 TKCKKPEPCDSCPCGECVACSCF-HGTLEPCRTNNTNCRKQSPRR-LMLTLIVL 178  
 DB 121 TKCKKPEPCDSCPCGECVACSCF-HGTLEPCRTNNTNCRKQSPRR-LMLTLIVL 178  
 QY 179 LIPLVFYRRYRRKCMRRDDPSRTSSRETIPMAASNLISLKYIPRIADMTIOEAK 238  
 DB 181 ALFVFLYKRYR-----KRGDSDESGISPESSPVNPNVSDNLKMYIMRAEMKICAK 235  
 QY 239 KFAENNIKEGKIDEIMHDSIQDTAEOKVOLLICMYOSHGKSDAYODLIFKIKAKRCRRT 298  
 DB 239 KFAENNIKEGKIDEIMHDSIQDTAEOKVOLLICMYOSHGKSDAYODLIFKIKAKRCRRT 298  
 QY 299 LDKPDMVOKDLKSTPTDGENEGOCLE 327  
 DB 299 LDKPDMVOKDLKSTPTDGENEGOCLE 327  
 QY 301 KPODMVOKDLKSTPTDGENEGOCLE 327  
 DB 301 KPODMVOKDLKSTPTDGENEGOCLE 327

## RESULT 3

A40036  
 Apoptosis-mediating surface antigen Fas precursor - human  
 N:Alternate names: surface antigen APO-1

C:Species: Homo sapiens (man)  
 C:Date: 17-Jan-1992 #sequence\_revision 17-Jan-1992 #text\_change 21-Jul-2000  
 C:Accession: A40036; S24543; A38142  
 R:Ridho, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Sameshima, M.;  
 Cell 66, 233-243, 1991  
 A:Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas can  
 A:Reference number: A40036; MUID:91309137; PMID:1713127  
 A:Accession: A40036  
 A:Molecule type: mRNA  
 A:Status: preliminary  
 A:Residues: 1-335 <IIO>  
 A:Cross-references: GB:M67454; NID:9182409; PID:AAA63174.1; PID:9182410  
 R:Kramer, P.H.  
 submitted to the EMBL Data Library, February 1992

A:Reference number: S24543  
 A:Accession: S24543  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-335 <RKAS>  
 A:Cross-references: EMBL:X63717; NID:928741; PID:928742  
 R:Oehm, A.; Behrmann, I.; Falk, M.; Pavlita, M.; Maier, G.; Klas, C.; Li-Weber, M.;  
 J. Biol. Chem. 267, 10709-10715, 1992  
 A:Title: Purification and molecular cloning of the APO-1 cell surface antigen, a member  
 A:Reference number: A38142; MUID:92268122; PMID:1375228  
 A:Accession: A38142  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: nucleic acid  
 A:Residues: 1-134, 'Q', 136-335 <OE>  
 A:Experimental source: SKW6.4 cells  
 A:Note: Sequence extracted from NCBI backbone (NCBIF:103810)  
 A:Note: In NCBI backbone the source is designated as mouse  
 C:Genetics:  
 A:Gene: GDB:APN1  
 A:Cross-references: GDB:132671; OMIM:134637  
 A:Map position: 10q24.1-10q24.1  
 C:Superfamily: NGF receptor repeat homology  
 C:Keywords: apoptosis; surface antigen; transmembrane protein  
 F:1-16/Domain: signal sequence #status predicted <SIG>  
 F:85-128/Domain: NGF receptor repeat homology <NGF>  
 F:174-190/Domain: transmembrane #status predicted <TM>

## Query Match

47.5% Score 856; DB 2: Length 335;  
 Best Local Similarity: 49.4% Pred. No. 4,86-54;  
 Matches 165; Conservative 54; Mismatches 107; Indels 8; Gaps 3;

QY 1 MIMTAVLPVLAGSGLRVHGTGNSISLKLRRVHETDKNCSEGLYOGGPFCC 56  
 DB 1 MIMTAVLPVLAGSGLRVHGTGNSISLKLRRVHETDKNCSEGLYOGGPFCC 56  
 QY 57 PGRKRVKDCCTTSGAFTCHPCTBEETDRKHSKCRCAFCDEGHELEVENCTRTON 116  
 DB 57 PGRKRVKDCCTTSGAFTCHPCTBEETDRKHSKCRCAFCDEGHELEVENCTRTON 116  
 QY 61 PGRKRVKDCCTTSGAFTCHPCTBEETDRKHSKCRCAFCDEGHELEVENCTRTON 120  
 DB 61 PGRKRVKDCCTTSGAFTCHPCTBEETDRKHSKCRCAFCDEGHELEVENCTRTON 120  
 QY 117 TKCKKPEPCDSCPCGECVACSCF-HGTLEPCRTNNTNCRKQSPRR-LMLTLIVL 176  
 DB 117 TKCKKPEPCDSCPCGECVACSCF-HGTLEPCRTNNTNCRKQSPRR-LMLTLIVL 176  
 QY 121 TKCKKPEPCDSCPCGECVACSCF-HGTLEPCRTNNTNCRKQSPRR-LMLTLIVL 180  
 DB 121 TKCKKPEPCDSCPCGECVACSCF-HGTLEPCRTNNTNCRKQSPRR-LMLTLIVL 180  
 QY 179 LIPLVFYRRYRRKCMRRDDPSRTSSRETIPMAASNLISLKYIPRIADMTIOEAK 232  
 DB 181 ALFVFLYKRYR-----KRGDSDESGISPESSPVNPNVSDNLKMYIMRAEMKICAK 230  
 QY 239 KFAENNIKEGKIDEIMHDSIQDTAEOKVOLLICMYOSHGKSDAYODLIFKIKAKRCRRT 292  
 DB 239 KFAENNIKEGKIDEIMHDSIQDTAEOKVOLLICMYOSHGKSDAYODLIFKIKAKRCRRT 292  
 QY 299 LDKPDMVOKDLKSTPTDGENEGOCLE 326  
 DB 299 LDKPDMVOKDLKSTPTDGENEGOCLE 326  
 QY 301 KPODMVOKDLKSTPTDGENEGOCLE 334  
 DB 301 KPODMVOKDLKSTPTDGENEGOCLE 334

## RESULT 4

I37383  
 Fas soluble protein - human